



SEQUENCE LISTING

<110> Evans, Glen A.

<120> Non-Immunoglobulin Binding Polypeptides

<130> 66663-026

<140> US 10/611,655

<141> 2003-06-30

<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 162

<212> PRT

<213> Homo sapiens

<400> 1

Met Asn Leu Ala Ile Ser Ile Ala Leu Leu Leu Thr Val Leu Gln Val
1 5 10 15
Ser Arg Gly Gln Lys Val Thr Ser Leu Thr Ala Cys Leu Val Asp Gln
20 25 30
Ser Leu Arg Leu Asp Cys Arg His Glu Asn Thr Ser Ser Ser Pro Ile
35 40 45
Gln Tyr Glu Glu Ser Leu Thr Arg Glu Thr Lys Lys His Val Leu Phe
50 55 60
Gly Thr Val Gly Val Pro Glu His Thr Tyr Arg Ser Arg Thr Asn Phe
65 70 75 80
Thr Ser Lys Tyr His Met Lys Val Leu Tyr Leu Ser Ala Phe Thr Ser
85 90 95
Lys Asp Glu Gly Thr Tyr Thr Cys Ala Leu His His Ser Gly His Ser
100 105 110
Pro Pro Ile Leu Ser Ser Gln Asn Val Thr Val Leu Arg Asp Lys Leu
115 120 125
Val Lys Cys Glu Gly Ile Ser Leu Leu Ala Gln Asn Thr Ser Trp Leu
130 135 140
Leu Leu Leu Leu Ser Leu Ser Leu Leu Gln Ala Thr Asp Phe Met
145 150 155 160
Ser Leu

<210> 2

<211> 124

<212> PRT

<213> Homo sapiens

<400> 2

Gln Leu Gln Gln Ser Gly Glu Ala Leu Val Lys Pro Gly Ala Ser Val

1	5	10	15
Arg Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Pro Asn Tyr Trp Met			
20	25	30	
His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Thr			
35	40	45	
Ile Asp Pro Ala Asp Ser Tyr Thr Ser Tyr Asn Gln Asn Phe Lys Asp			
50	55	60	
Lys Ala Thr Leu Thr Val Lys Pro Ser Ser Thr Ala Tyr Met Gln Leu			
65	70	75	80
Ser Ser Leu Thr Phe Gly Asp Ser Ala Val Tyr Phe Cys Ala Arg Glu			
85	90	95	
Ser Tyr Tyr Tyr Arg Tyr Phe Asp Tyr Trp Gly His Gly Thr Thr			
100	105	110	
Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Lys Leu			
115	120		

<210> 3

<211> 37

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus peptide

<400> 3

Gln Leu Ser Leu Lys Leu Cys Lys Ser Ser Phe Arg Gly Thr Ile Asp			
1	5	10	15
Asn Phe Lys Asp Ala Thr Thr Ser Ile Ser Ser Glu Gly Ile Trp Leu			
20	25	30	
Ser Leu Ser Thr Leu			
35			

<210> 4

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> ThyOx non-immunoglobulin binding polypeptide

<400> 4

Gln Val Ser Arg Gly Gln Lys Val Thr Ser Leu Thr Ala Cys Leu Val			
1	5	10	15
Asp Gln Ser Leu Arg Leu Asp Cys Arg His Glu Asn Thr Ser Ser Ser			
20	25	30	
Asn Tyr Trp Met His Phe Ser Leu Thr Arg Glu Thr Lys Lys His Val			
35	40	45	
Leu Phe Gly Thr Ile Asp Pro Ala Asp Ser Tyr Thr Ser Tyr Asn Gln			
50	55	60	
Asn Phe Lys Asp Glu Gly Thr Tyr Thr Cys Ala Leu His His Ser Gly			
65	70	75	80
His Ser Pro Pro Ile Ser Ser Gln Asn Val Thr Val Leu Arg Asp Lys			
85	90	95	

Leu Val Lys Cys Glu Gly Val Tyr Tyr Arg Tyr Tyr Phe Asp Tyr
100 105 110

<210> 5
<211> 1050
<212> DNA
<213> Artificial Sequence

<220>
<223> carrier encoding erythropoietin

<221> CDS
<222> (21) ... (1022)

<400> 5
gattggcgaa gcttggagga atg ggc gtg cac gag tgc ccc gcc tgg ctg tgg 53
Met Gly Val His Glu Cys Pro Ala Trp Leu Trp
1 5 10

ctg ctg ctg agc ctg ctg agc ctg ccc ctg ggc ctg ccc gtg ctg ggc 101
Leu Leu Leu Ser Leu Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly
15 20 25

gcc ccc ccc cgg ctg atc tgc gac agc cgg gtg ctg gag cgg cac ctg 149
Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg His Leu
30 35 40

ctg gag gcc aag gag gcc gag agc atc acc acc ggc tgc gtg gag gac 197
Leu Glu Ala Lys Glu Ala Glu Ser Ile Thr Thr Gly Cys Val Glu Asp
45 50 55

tgc agc ctg aac gag aac atc acc acc gtg ccc gac agc aag gtg aac ttc 245
Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Ser Lys Val Asn Phe
60 65 70 75

tac gcc tgg aag cgg atg gag gtg ggc cag cag gcc gtg gag gtg tgg 293
Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
80 85 90

cag ggc ctg gcc ctg ctg agc gag gcc gtg ctg cgg ggc cag gcc ctg 341
Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
95 100 105

ctg gtg atc agc agc cag ccc tgg gag ccc ctg cag ctg cac gtg gac 389
Leu Val Ile Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
110 115 120

aag gcc gtg agc ggc ctg cgg agc ctg acc acc ctg ctg cgg gcc ctg 437
Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
125 130 135

ggc gcc cag aag gag gcc atc agc ccc ccc gac gcc gcc agc gcc ggc 485
Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala

140	145	150	155	
ccc ctg cgg acc atc acc gcc gac acc ttc cgg aag ctg ttc cgg gtg				533
Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val				
160	165	170		
tac ccc aac ttc ctg cgg ggc aag ctg aag ttc tac acc ggc gag gcc				581
Tyr Pro Asn Phe Leu Arg Gly Lys Leu Lys Phe Tyr Thr Gly Glu Ala				
175	180	185		
tgc cgg ggc ggc ggc ggc agc ggc ggc ggc ggc gag ttc ggc ggc				629
Cys Arg Gly Gly Gly Ser Gly Gly Gly Glu Phe Gly Gly				
190	195	200		
ggc ggc agc cag aag gtg acc agc ctg acc gcc tgc ctg gtg gac cag				677
Gly Gly Ser Gln Lys Val Thr Ser Leu Thr Ala Cys Leu Val Asp Gln				
205	210	215		
agc ctg cgg ctg gac tgc cgg cac gag aac acc agc agc agc ccc atc				725
Ser Leu Arg Leu Asp Cys Arg His Glu Asn Thr Ser Ser Ser Pro Ile				
220	225	230	235	
cag tac gag ttc agc ctg acc cgg gag acc aag aac cac gtg ctg ttc				773
Gln Tyr Glu Phe Ser Leu Thr Arg Glu Thr Lys Lys His Val Leu Phe				
240	245	250		
ggc acc gtg ggc gtg ccc gag cac acc tac cgg agc cgg acc aac ttc				821
Gly Thr Val Gly Val Pro Glu His Thr Tyr Arg Ser Arg Thr Asn Phe				
255	260	265		
acc agc aag tac cac atg aag gtg ctg tac ctg agc gcc ttc acc agc				869
Thr Ser Lys Tyr His Met Lys Val Leu Tyr Leu Ser Ala Phe Thr Ser				
270	275	280		
aag gac gag ggc acc tac acc tgc gcc ctg cac cac agc ggc cac agc				917
Lys Asp Glu Gly Thr Tyr Cys Ala Leu His His Ser Gly His Ser				
285	290	295		
ccc ccc atc agc agc cag aac gtg acc gtg ctg cgg gac aag ctg gtg				965
Pro Pro Ile Ser Ser Gln Asn Val Thr Val Leu Arg Asp Lys Leu Val				
300	305	310	315	
aag tgc gag ggc atc agc ctg ctg gcc cag aac acc agc cac cac cac				1013
Lys Cys Glu Gly Ile Ser Leu Leu Ala Gln Asn Thr Ser His His His				
320	325	330		
cac cac cac tgatgataag atcggatcct aggcttcc				1050
His His His				

<210> 6

<211> 334

<212> PRT

<213> Artificial Sequence

<220>

<223> chimeric ThyOx carrier polypeptide containing
erythropoietin

<400> 6

Met	Gly	Val	His	Glu	Cys	Pro	Ala	Trp	Leu	Trp	Leu	Leu	Leu	Ser	Leu
1				5					10					15	
Leu	Ser	Leu	Pro	Leu	Gly	Leu	Pro	Val	Leu	Gly	Ala	Pro	Pro	Arg	Leu
						20			25					30	
Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	His	Leu	Leu	Glu	Ala	Lys	Glu
						35			40			45			
Ala	Glu	Ser	Ile	Thr	Thr	Gly	Val	Glu	Asp	Cys	Ser	Leu	Asn	Glu	
			50				55				60				
Asn	Ile	Thr	Val	Pro	Asp	Ser	Lys	Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg
			65				70			75				80	
Met	Glu	Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp	Gln	Gly	Leu	Ala	Leu
						85			90			95			
Leu	Ser	Glu	Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu	Leu	Val	Ile	Ser	Ser
						100			105			110			
Gln	Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp	Lys	Ala	Val	Ser	Gly
						115			120			125			
Leu	Arg	Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu	Gly	Ala	Gln	Lys	Glu
			130				135				140				
Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala	Pro	Leu	Arg	Thr	Ile
			145				150				155			160	
Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val	Tyr	Pro	Asn	Phe	Leu
						165			170			175			
Arg	Gly	Lys	Leu	Lys	Phe	Tyr	Thr	Gly	Glu	Ala	Cys	Arg	Gly	Gly	Gly
						180			185			190			
Gly	Gly	Ser	Gly	Gly	Gly	Glu	Phe	Gly	Gly	Gly	Ser	Gln	Lys		
						195			200			205			
Val	Thr	Ser	Leu	Thr	Ala	Cys	Leu	Val	Asp	Gln	Ser	Leu	Arg	Leu	Asp
						210			215			220			
Cys	Arg	His	Glu	Asn	Thr	Ser	Ser	Ser	Pro	Ile	Gln	Tyr	Glu	Phe	Ser
						225			230			235			240
Leu	Thr	Arg	Glu	Thr	Lys	Lys	His	Val	Leu	Phe	Gly	Thr	Val	Gly	Val
						245			250			255			
Pro	Glu	His	Thr	Tyr	Arg	Ser	Arg	Thr	Asn	Phe	Thr	Ser	Lys	Tyr	His
						260			265			270			
Met	Lys	Val	Leu	Tyr	Leu	Ser	Ala	Phe	Thr	Ser	Lys	Asp	Glu	Gly	Thr
						275			280			285			
Tyr	Thr	Cys	Ala	Leu	His	His	Ser	Gly	His	Ser	Pro	Pro	Ile	Ser	Ser
						290			295			300			
Gln	Asn	Val	Thr	Val	Leu	Arg	Asp	Lys	Leu	Val	Lys	Cys	Glu	Gly	Ile
						305			310			315			320
Ser	Leu	Leu	Ala	Gln	Asn	Thr	Ser	His							
						325			330						

<210> 7

<211> 1050

<212> DNA

<213> Artificial Sequence

<220>

<223> SuperEpo

<221> CDS

<222> (21) ... (1022)

<400> 7

gattggcgaa	gcttggagga	atg	ggc	gtg	cac	gag	tgc	ccc	gcc	tgg	ctg	tgg	53
		Met	Gly	Val	His	Glu	Cys	Pro	Ala	Trp	Leu	Trp	
		1			5						10		

ctg	ctg	ctg	agc	ctg	agc	ccc	ctg	ggc	ctc	ccc	gtg	ctg	ggc	101
Leu	Leu	Leu	Ser	Leu	Leu	Ser	Leu	Pro	Leu	Gly	Leu	Pro	Val	
15							20					25		

gcc	ccc	ccc	cg	ctg	atc	tgc	gac	agc	cg	gtg	ctg	qag	cg	cac	ctg	149
Ala	Pro	Pro	Arg	Leu	Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	His	Leu	
30							35					40				

ctg	gag	gcc	aag	gag	gcc	gag	agc	atc	acc	acc	ggc	tgc	gtg	gag	gac	197
Leu	Glu	Ala	Lys	Glu	Ala	Glu	Ser	Ile	Thr	Thr	Gly	Cys	Val	Glu	Asp	
45							50					55				

tgc	agc	ctg	aac	gag	aac	atc	acc	gtg	ccc	gac	agc	aag	gtg	aac	ttc	245
Cys	Ser	Leu	Asn	Glu	Asn	Ile	Thr	Val	Pro	Asp	Ser	Lys	Val	Asn	Phe	
60							65					70			75	

tac	gcc	tgg	aag	cg	atg	gag	gtg	ggc	cag	cag	gcc	gtg	gag	gtg	tgg	293
Tyr	Ala	Trp	Lys	Arg	Met	Glu	Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp	
80							85					90				

cag	ggc	ctg	gcc	ctg	ctg	agc	gag	gcc	gtg	ctg	cg	ggc	cag	gcc	ctg	341
Gln	Gly	Leu	Ala	Leu	Leu	Ser	Glu	Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu	
95							100					105				

ctg	gtg	atc	agc	agc	cag	ccc	tgg	gag	ccc	ctg	cag	ctg	cac	gtg	gac	389
Leu	Val	Ile	Ser	Ser	Gln	Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp	
110							115					120				

aag	gcc	gtg	agc	ggc	ctg	cg	agc	ctg	acc	acc	ctg	ctg	cg	ggc	ctg	437
Lys	Ala	Val	Ser	Gly	Leu	Arg	Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu	
125							130					135				

ggc	ggc	cag	aag	gag	gcc	atc	agc	ccc	ccc	gac	gcc	agc	gcc	ggc	485	
Gly	Ala	Gln	Lys	Glu	Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala	
140							145					150			155	

ccc	ctg	cg	acc	atc	acc	gcc	gac	acc	ttc	cg	aag	ctg	ttc	cg	gtg	533
Pro	Leu	Arg	Thr	Ile	Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val	
160							165					170				

tac ccc aac ttc ctg cg ^g ggc aag ctg aag ttc tac acc ggc gag gcc	581		
Tyr Pro Asn Phe Leu Arg Gly Lys Leu Lys Phe Tyr Thr Gly Glu Ala			
175	180	185	
tgc cg ^g ggc ggc ggc ggc agc gg ^g ggc gg ^g ggc gag ttc ggc ggc	629		
Cys Arg Gly Gly Gly Ser Gly Gly Gly Glu Phe Gly Gly			
190	195	200	
ggc ggc agc cag aag gtg acc agc ctg acc gcc tgc ctg gtg gac cag	677		
Gly Gly Ser Gln Lys Val Thr Ser Leu Thr Ala Cys Leu Val Asp Gln			
205	210	215	
agc ctg cg ^g ctg gac tgc cg ^g cac gag aac acc agc agc ccc atc	725		
Ser Leu Arg Leu Asp Cys Arg His Glu Asn Thr Ser Ser Ser Pro Ile			
220	225	230	235
cag tac gag ttc agc ctg acc cg ^g gag acc aag aag cac gtg ctg ttc	773		
Gln Tyr Glu Phe Ser Leu Thr Arg Glu Thr Lys Lys His Val Leu Phe			
240	245	250	
ggc acc gtg ggc gtg ccc gag cac acc tac cg ^g agc cg ^g acc aac ttc	821		
Gly Thr Val Gly Val Pro Glu His Thr Tyr Arg Ser Arg Thr Asn Phe			
255	260	265	
acc agc aag tac cac atg aag gtg ctg tac ctg agc gcc ttc acc agc	869		
Thr Ser Lys Tyr His Met Lys Val Leu Tyr Leu Ser Ala Phe Thr Ser			
270	275	280	
aag gac gag ggc acc tac acc tgc gcc ctg cac cac agc ggc cac agc	917		
Lys Asp Glu Gly Thr Tyr Cys Ala Leu His His Ser Gly His Ser			
285	290	295	
ccc ccc atc agc agc cag aac gtg acc gtg ctg cg ^g gac aag ctg gtg	965		
Pro Pro Ile Ser Ser Gln Asn Val Thr Val Leu Arg Asp Lys Leu Val			
300	305	310	315
aag tgc gag ggc atc agc ctg ctg gcc cag aac acc agc cac cac cac	1013		
Lys Cys Glu Gly Ile Ser Leu Leu Ala Gln Asn Thr Ser His His His			
320	325	330	
cac cac cac tgatgataag atcggatcct aggttcc	1050		
His His His			

<210> 8
<211> 334
<212> PRT
<213> Artificial Sequence

<220>
<223> SuperEpo

<400> 8

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
1 5 10 15
Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
20 25 30
Ile Cys Asp Ser Arg Val Leu Glu Arg His Leu Leu Glu Ala Lys Glu
35 40 45
Ala Glu Ser Ile Thr Thr Gly Cys Val Glu Asp Cys Ser Leu Asn Glu
50 55 60
Asn Ile Thr Val Pro Asp Ser Lys Val Asn Phe Tyr Ala Trp Lys Arg
65 70 75 80
Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
85 90 95
Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Ile Ser Ser
100 105 110
Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
115 120 125
Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
130 135 140
Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
145 150 155 160
Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Pro Asn Phe Leu
165 170 175
Arg Gly Lys Leu Lys Phe Tyr Thr Gly Glu Ala Cys Arg Gly Gly Gly
180 185 190
Gly Gly Ser Gly Gly Gly Glu Phe Gly Gly Gly Ser Gln Lys
195 200 205
Val Thr Ser Leu Thr Ala Cys Leu Val Asp Gln Ser Leu Arg Leu Asp
210 215 220
Cys Arg His Glu Asn Thr Ser Ser Pro Ile Gln Tyr Glu Phe Ser
225 230 235 240
Leu Thr Arg Glu Thr Lys Lys His Val Leu Phe Gly Thr Val Gly Val
245 250 255
Pro Glu His Thr Tyr Arg Ser Arg Thr Asn Phe Thr Ser Lys Tyr His
260 265 270
Met Lys Val Leu Tyr Leu Ser Ala Phe Thr Ser Lys Asp Glu Gly Thr
275 280 285
Tyr Thr Cys Ala Leu His His Ser Gly His Ser Pro Pro Ile Ser Ser
290 295 300
Gln Asn Val Thr Val Leu Arg Asp Lys Leu Val Lys Cys Glu Gly Ile
305 310 315 320
Ser Leu Leu Ala Gln Asn Thr Ser His His His His His His His
325 330

<210> 9

<211> 600

<212> DNA

<213> Artificial Sequence

<220>

<223> carrier encoding glucagon-like peptide 1

<221> CDS

<222> (29)...(556)

<400> 9

agtccgggat ttaagaattc agctgtcc atg cac ggt gaa ggt acc ttc acc 52
Met His Gly Glu Gly Thr Phe Thr
1 5

tct gac gtt tct tac ctg gaa ggt cag gcg aaa gag ttc atc 100
Ser Asp Val Ser Ser Tyr Leu Glu Gly Gln Ala Ala Lys Glu Phe Ile
10 15 20

gcg tgg ctg gtt aaa ggt cgt ggt ggt ggt tct ggt ggt ggt 148
Ala Trp Leu Val Lys Gly Arg Gly Gly Ser Gly Gly Gly
25 30 35 40

ggt gag ttc ggt ggt tct cag aaa gtt acc tct ctg acc gcg 196
Gly Glu Phe Gly Gly Ser Gln Lys Val Thr Ser Leu Thr Ala
45 50 55

tgc ctg gtt gac cag tct ctg cgt ctg gac tgc cgt cac gaa aac acc 244
Cys Leu Val Asp Gln Ser Leu Arg Leu Asp Cys Arg His Glu Asn Thr
60 65 70

tct tct tct ccg atc cag tac gag ttc tct ctg acc cgt gaa acc aaa 292
Ser Ser Ser Pro Ile Gln Tyr Glu Phe Ser Leu Thr Arg Glu Thr Lys
75 80 85

aaa cac gtt ctg ttc ggt acc gtt ggt ccg gaa cac acc tac cgt 340
Lys His Val Leu Phe Gly Thr Val Gly Val Pro Glu His Thr Tyr Arg
90 95 100

tct cgt acc aac ttc acc tct aaa tac cac atg aaa gtt ctg tac ctg 388
Ser Arg Thr Asn Phe Thr Ser Lys Tyr His Met Lys Val Leu Tyr Leu
105 110 115 120

tct gcg ttc acc tct aaa gac gaa ggt acc tac acc tgc gcg ctg cac 436
Ser Ala Phe Thr Ser Lys Asp Glu Gly Thr Tyr Thr Cys Ala Leu His
125 130 135

cac tct ggt cac tct ccg atc tct tct cag aac gtt acc gtt ctg 484
His Ser Gly His Ser Pro Pro Ile Ser Ser Gln Asn Val Thr Val Leu
140 145 150

cgt gac aaa ctg gtt aaa tgc gaa ggt atc tct ctg ctg gcg cag aac 532
Arg Asp Lys Leu Val Lys Cys Glu Gly Ile Ser Leu Leu Ala Gln Asn
155 160 165

acc tct cac cac cac cac tgataatgag atcttgaggc cggtatccgct 586
Thr Ser His His His His His
170 175

taagatccccg gcaa 600

<210> 10
<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<223> chimeric ThyOx carrier polypeptide containing
glucagon-like peptide 1

<400> 10
Met His Gly Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu
1 5 10 15
Gly Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
20 25 30
Gly Gly Gly Ser Gly Gly Gly Glu Phe Gly Gly Gly Ser
35 40 45
Gln Lys Val Thr Ser Leu Thr Ala Cys Leu Val Asp Gln Ser Leu Arg
50 55 60
Leu Asp Cys Arg His Glu Asn Thr Ser Ser Pro Ile Gln Tyr Glu
65 70 75 80
Phe Ser Leu Thr Arg Glu Thr Lys Lys His Val Leu Phe Gly Thr Val
85 90 95
Gly Val Pro Glu His Thr Tyr Arg Ser Arg Thr Asn Phe Thr Ser Lys
100 105 110
Tyr His Met Lys Val Leu Tyr Leu Ser Ala Phe Thr Ser Lys Asp Glu
115 120 125
Gly Thr Tyr Thr Cys Ala Leu His His Ser Gly His Ser Pro Pro Ile
130 135 140
Ser Ser Gln Asn Val Thr Val Leu Arg Asp Lys Leu Val Lys Cys Glu
145 150 155 160
Gly Ile Ser Leu Leu Ala Gln Asn Thr Ser His His His His His
165 170 175

<210> 11
<211> 4000
<212> DNA
<213> Artificial Sequence

<220>
<223> vector pEgea M3

<400> 11
gattattctt gacccgcgtt acataactt cggtaaatgg cccgcctggc tgaccgcccc 60
acgacccccc cccattgacg tcaataatga cgtatgttcc catagtaacg ccaataggga 120
ctttccattt acgtcaatgg gtggagtatt tacgttaaac tgcccacttg gcagtacatc 180
aagtgtatca tatgccaagt acgcccccta ttgacgtcaa tgacggtaaa tggcccgct 240
ggcattatgc ccagtacatg accttatggg acttcctac ttggcagtagc atctacgtat 300
tagtcatcgc tattaccatg gtgatgcggt tttggcagta catcaatggg cgtggatagc 360
ggtttactc acggggattt ccaagtctcc acccattga cgtcaatggg agtttgttt 420
ggcaccaaaa tcaacgggac tttccaaaat gtcgtacaa ctccgcccc ttgacgcaaa 480
tgggcggtag gcgtgtacgg tgggaggtct atataagcag agctctctgg ctaactagaa 540
tcgaaattaa tacgactcac tatagggaga cccaaagctgg ctacgcgttta aacttaagct 600

tggtaaccgag	ctcgatcca	ctctaggggg	tatccccacg	cgccctgtag	cgccgcatta	660
agcgcggcgg	gtgtgggt	tacgcgcagc	gtgaccgcta	cacttgcacag	cgccctagcg	720
cccgctcctt	tcgcttctt	cccttcctt	ctcgccacgt	tcgcccgtt	tccccgtcaa	780
gctctaaatc	gggggctccc	tttagggttc	cgatttagtg	cttacggca	cctcgacccc	840
aaaaaaactt	attagggta	tggttacagt	agtggccat	cgccctgata	gacggttttt	900
cgcccttga	cggtggagtc	cacgttctt	aatagtggac	tcttggcca	aactggaaaca	960
acactcaacc	ctatctcggt	ctattcttt	gatttataag	ggatttgcc	gatttcggcc	1020
tattggtaa	aaaatgagct	gatthaacaa	aaatthaacg	cgaattaatt	ctgtggaaatg	1080
tgtgtcagtt	agggtgtgga	aagtccccag	gctcccccagc	aggcagaagt	atgcaaagca	1140
tgcacatctca	ttagttagc	accagggtgt	gaaagtcccc	aggctcccca	gcaggcagaa	1200
gtatgcaaag	catgcacatc	aatttagtcag	caaccatagt	cccgccccca	actccgcccc	1260
tcccgcccc	aactccgccc	agttccgccc	attctccgccc	ccatggctga	ctaatttttt	1320
ttatttatgc	agagggccgag	ggccgcctcg	cctctgagct	attccagaag	tagtgaggag	1380
gctttttgg	aggcctaggg	ttttgcaaaaa	agctcgagga	tcgttgcga	tgattgaaca	1440
agatggattt	cacgcagggtt	ctccggccgc	ttgggtggag	aggctattcg	gctatgactg	1500
ggcacaacag	acaatccgct	gctctgtatgc	cgccgtgttc	cggtgtcag	cgccaggggcg	1560
cccggttctt	tttgtaaga	ccgacctgtc	cggtgcctg	aatgaactgc	aggacgaggc	1620
agcgcggcta	tcgtggctgg	ccacgacggg	cgttccttgc	gcagctgtgc	tcgacgttgt	1680
cactgaagcg	ggaaggggact	ggctgtatt	gggcgaagtg	ccggggcagg	atctcctgtc	1740
atctcacctt	gctccgtccg	agaaagtatc	catcatggct	gatgcaatgc	ggccgctgca	1800
tacgcttgc	ccggctaccc	gcccattcga	ccaccaagcg	aaacatcgca	tcgagcgagc	1860
acgtactcgg	atggaagccg	gtcttgcga	tcaggatgt	ctggacgaag	agcatcaggg	1920
gctcgcgc	gccgaactgt	tcgcccaggt	caaggcgcgc	atgcccgcag	gcccggatct	1980
cgtcgtgacc	catggcgatg	cctgcttgc	aatatcatg	gtggaaaatg	gccgcttttc	2040
tggattcatc	gactgtggcc	ggctgggtgt	ggcggaccgc	tatcaggaca	tagcgttggc	2100
tacccgtat	attgtcgaag	agcttggcgg	cgaatggct	gaccgcttcc	tcgtgcttta	2160
cggtatcgcc	gctcccgatt	cgcagcgcatt	cgccttctat	cgccttcttgc	acgagttctt	2220
ctgagcggga	cgcaccccaa	tttgcattt	gcagcttata	atggttacaa	ataaaagcaat	2280
agcatcaca	atttcacaaa	taaagcattt	tttcactgc	attctagtttgc	tgggttgc	2340
aaactcatca	atgtatctta	tcatgtctgt	ataccgtcga	cctctagcta	atgtgagcaa	2400
aaggccagca	aaaggccagg	aaccgtaaaa	aggccgcgtt	gctggcggtt	ttccataggc	2460
tccggcccc	tgacgagcat	cacaaaaatc	gacgctcaag	tcagagggtgg	cgaaaccgcga	2520
caggactata	aagataccag	gcgttcccc	ctggaaagctc	cctcgtgcgc	tctcctgttc	2580
cgaccctgc	gcttaccgg	tacctgtcc	ccttctccc	ttcgggaagc	gtggcgcttt	2640
ctcatagctc	acgctgttagg	tatctcagg	cggtgttaggt	cggtcgctcc	aagctgggt	2700
gtgtgcacga	accccccgtt	cagcccgacc	gctgcgcctt	atccggtaac	tatcgtcttgc	2760
agtccaaacc	ggtaaagacac	gacttatcgc	cactggcagc	agccactgg	aacaggatta	2820
gcagagcgag	gtatgttaggc	ggtgctacag	agttcttgc	gtgggtggc	aactacggct	2880
acactagaag	aacagtat	ggtatctgc	ctctgctgaa	gccagttacc	ttcggaaaaaa	2940
gagttggtag	ctcttgcattc	gccaaacaaa	ccaccgctgg	tagcggtttt	tttgcattc	3000
agcagcagat	tacgcgcaga	aaaaaaaggat	ctcaagaaga	tcctttgatc	ttttctacgg	3060
ggctgtacgc	tcagtgaaac	aaaaaccagt	taccaatgc	taatcgtga	ggcacctatc	3120
tcagcgatct	gtctatttgc	ttcatccata	gttgcctgac	tccccgtcgt	gtagataact	3180
acgatacggg	agggcttacc	atctggcccc	agtgtcgtt	tgataccgc	agacccacgc	3240
tcaccggctc	cagatttac	agcaataaac	cagccagccg	gaagggccga	gcgcagaagt	3300
ggtcctgcaa	ctttatccgc	ctccatccag	tctattaatt	gttgcggg	agctagagta	3360
agtagttcgc	cagttatag	tttgcgcac	gttgggttgc	ttgctacagg	catcgtgg	3420
tcacgctcgt	cgtttggat	gcttcattc	agctccgg	cccaacgatc	aaggcgagtt	3480
acatgatccc	ccatgttgc	aaaaaaagcg	gttagcttgc	tcggcctcc	gatcggttgc	3540
agaagtaagt	tggccgcagt	gttacactc	atggttatgg	cagcactgca	taattctt	3600
actgtcatgc	cacccgtaa	atgcttttgc	gtgactgg	agtactcaac	caagtcatc	3660
tgagaatagt	gtatgcggcg	accgagttgc	tcttgcgg	cgtcaatacg	ggataatacc	3720
cgcccacata	cgagaactt	aaaagtgc	atcattggaa	aacgttcttgc	ggggcgaaaa	3780

ctctcaagga tcttaccgct gttgagatcc agttcgatgt aacccactcg tgcacccaaac	3840
tgatcttcag catctttac tttcaccagc gtttctgggt gagcaaaaac aggaaggcaa	3900
aatggcgcaa aaaagggaaat aaggggcgaca cgaaaaatgtt gaataactcat actcttcctt	3960
tttcaatatt attqaaqcat ttatctqaqg qttattqtct	4000

<210> 12
<211> 1750
<212> DNA
<213> Artificial Sequence

<220>
<223> vector pEgea Q6

<400> 12
agtgccttag acctgttgac aattaatcat cggctcgat aatgtgtgga attgtgagcg
gataacaatt tcacacagga aacaggatcg atcgaattcg gatccaagct tgagctcgag
ccatggcccg ggtgaataat tagaaaagat caaaggatct tcttgagatc cttttttct
gcgcgtaatc tgctgcttgc aaacaaaaaa accaccgcta ccagcggtgg tttgtttgcc
ggatcaagag ctaccaactc ttttccgaa ggtaactggc tttagcagag cgccagatacc
aaatactgtt cttagtgcgtagt aggccaccac ttcaagaact ctgttagcacc
gcctacatac ctcgctctgc taatcctgtt accagtggct gctgccagtg gcgataagtc
gtgtcttacc gggttggact caagacgata gttaccggat aaggcgcagc ggtcgccgt
aacggggggt tcgtgcacac agcccgaccc ggagcgaacg acctacaccg aactgagata
cctacagcgt gagctatgag aaagcgccac gttcccgaa gggacaaagg cggacaggt
tccggtaagc ggcagggtcg gaacaggaga ggcacacggg gagctccag ggggaaacgc
ctggtatctt tatagtcctg tcgggttgc ccacctotga ctttagcgtc gatTTTGTG
atgctcgtaa gggggcgga gcctatggaa aaacgcccac aacgcggcct tttacggtt
cctgcccgt cattaggcgg gctattacca atgcttaatc agtgaggcac ctatctcagc
gatctgtcta tttcggtcat ccatacgatgc ctgactcccc gtcgtgtaga taactacgat
acgggggggc ttaccatctg gccccagtc tgcaatgata cccgcgagacc cacgctcacc
ggctccagat ttatcagcaa taaaaccagcc agccggaaagg gccgagcga gaagtggtcc
tgcaacttta tccgcctcca tccagtttat taattgttgc cgggaagcta gagtaagttag
ttcgccagtt aatagtttgc gcaacgttgc tgccattgtc acaggcatcg tgggtgtcacg
ctcgctgttt ggtatggcctt cattcagtc cgggtcccaa cgatcaaggc gagttacatg
atccccatg ttgtcaaaaa aagcggttag ctccctcggt cctccgatcg ttgtcagaag
taagttggcc gcagtgttat cactcatggt tatggcagca ctgcataatt ctcttactgt
catgccatcc gtaagatgct tttctgtgac tgggtgagtc tcaaccaagt cattctgaga
atagtgtatg cggcgaccga gttgctcttgc cccggcgtca atacgggata ataccgcgcc
acatagcaga actttaaaag tgctcatcat tggaaaacgt tcttcggggc gaaaactctc
aaggatctt ccgcgttgc gatccagttc gatgttaaccc actcgtgctc ccaactgatc
ttcagcatct ttactttca ccagcgttgc tgggtgagca aaaacaggaa ggcaaaaatgc
cgaaaaaaag ggaataaggcgacacggaa atgttgaata ctcatactct tccttttca
atattattga agcatttatac agggttatttgc tctcatgagc ggatacatat ttgaatgtat
ctagaaggt

<210> 13
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic linker

<400> 13
ggggsggggs ggggs

15



Document: Sequence Listing pages 1-13

Attorney Client-Matter No: 66663-026
(P-EA 5191)

CERTIFICATE OF MAILING BY "EXPRESS MAIL"

"EXPRESS MAIL" MAILING LABEL NUMBER: EV 40171127 US

DATE OF DEPOSIT: December 15, 2003

I HEREBY CERTIFY THAT THIS PAPER OR FEE IS BEING DEPOSITED WITH THE UNITED STATES POSTAL SERVICE "EXPRESS MAIL POST OFFICE TO ADDRESSEE" SERVICE UNDER 37 CFR 1.10 ON THE DATE INDICATED ABOVE AND IS ADDRESSED TO MAIL STOP MISSING PARTS, COMMISSIONER FOR PATENTS, P.O. BOX 1450, ALEXANDRIA, VA 22313-1450.

Paul Cho:

Printed Name of Person Mailing Paper or Fee



Signature of Person Mailing Paper or Fee